

Boo

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Details

 **1: Z81449. Caenorhabditis el...**[\[gi:1658303\]](#) [Links](#)

It may be shorter because we only sequence overlapping sections

once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone C46F11 is at 45409 in sequence Z48241.

The true right end of clone C46F11 is at 8174 in sequence Z48245.

The start of this sequence (1..102) overlaps with the end of sequence Z48241.

The end of this sequence (34740..34841) overlaps with the start of sequence Z48245.

FEATURES

	Location/Qualifiers
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ORIGIN

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34201 cattttttga tatcgactag aacaatttag ttaaactctg tcgtcaaagt tgatcctaac
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34681 tgggaggaat caatttgctt cgaaatctca aagtttcggg aaatttctaa tattttttaa
34741 tgcaaaattt tggctgaaat tcgggggttt gaggggtttt tttaatgaaa aaaatagcat
34801 ttgaaaaact gaagttcatg agcttccgga tgacgttaaa a
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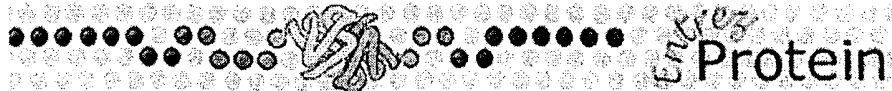
May 6 2004 12:36:28

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1741 cggaattc

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1: P09052[gi:1352826] This record was replaced or removed. See revision history for details.

LOCUS P09052 661 aa linear INV 01-FEB-1996

DEFINITION VASA PROTEIN.

ACCESSION P09052

VERSION P09052 GI:1352826

DBSOURCE swissprot: locus VASA_DROME, accession P09052;

class: standard.

created: Nov 1, 1988.

sequence updated: Feb 1, 1996.

annotation updated: Feb 1, 1996.

xrefs: gi: 433675, gi: 1054723, gi: 8804, gi: 84895, gi: 84894

xrefs (non-sequence databases): FLYBASEFBgn0003970, PFAMPF00270,

PFAMPF00271, PROSITEPS00039

KEYWORDS Developmental protein; ATP-binding; Repeat; Helicase.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (residues 1 to 661)

AUTHORS Lasko,P.F. and Ashburner,M.

TITLE The product of the Drosophila gene vasa is very similar to

eukaryotic initiation factor-4A

JOURNAL Nature 335 (6191), 611-617 (1988)

MEDLINE 89014721

REMARK SEQUENCE FROM N.A.

REFERENCE 2 (residues 1 to 661)

AUTHORS LASKO,P.F.

TITLE Direct Submission

JOURNAL Submitted (~DEC-1993)

REMARK REVISIONS.

REFERENCE 3 (residues 1 to 661)

AUTHORS Hay,B., Jan,L.Y. and Jan,Y.N.

TITLE A protein component of Drosophila polar granules is encoded by vasa

and has extensive sequence similarity to ATP-dependent helicases

JOURNAL Cell 55 (4), 577-587 (1988)

MEDLINE 89028669

REMARK SEQUENCE FROM N.A.

COMMENT [WARNING] On Feb 1, 2001 this sequence was replaced by a newer

version gi:12644110.

On Jun 4, 1996 this sequence version replaced gi:137452.

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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
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and <http://www.ebi.ac.uk/sprot>

[FUNCTION] THE VASA PROTEIN IS REQUIRED ONLY IN THE FEMALE GERM
LINE. IT IS IMPORTANT FOR OOCYTE FORMATION AND IN THE SPECIFICATION
OF THE POSTERIOR STRUCTURES OF THE EMBRYO.

[DEVELOPMENTAL STAGE] MATERNALLY EXPRESSED (DURING OOGENESIS).
FUNCTION DURING EARLY EMBRYOGENESIS.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES.

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FEATURES             Location/Qualifiers
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                       /db_xref="taxon:7227"
    gene              1..661
                       /gene="VAS"
    Protein           1..661
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                       /product="VASA PROTEIN"
    Region            35
                       /gene="VAS"
                       /region_name="Conflict"
                       /note="A -> R (IN REF. 3)."
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Region 93..127

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                       /region_name="Domain"
                       /note="5 X 7 AA TANDEM REPEATS OF [FS]-R-G-G- [EQ]-G-G."
    Region            93..99
                       /gene="VAS"
                       /region_name="Repetitive region"
                       /note="1."
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Region 100..106

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                       /region_name="Repetitive region"
                       /note="2."
    Region            107..113
                       /gene="VAS"
                       /region_name="Repetitive region"
                       /note="3."
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Region 114..120

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                       /region_name="Repetitive region"
                       /note="4."
    Region            121..127
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                       /region_name="Repetitive region"
                       /note="5."
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Region 265

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                       /region_name="Conflict"
                       /note="F -> Y (IN REF. 3)."
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Site 289..296

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                       /gene="VAS"
                       /site_type="np-binding"
                       /note="ATP (BY SIMILARITY)."
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Site 399..402

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                       /gene="VAS"
                       /site_type="unclassified"
                       /note="DEAD BOX."
    Region            582
                       /gene="VAS"
                       /region_name="Conflict"
                       /note="C -> R (IN REF. 3)."
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Region 594

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                       /gene="VAS"
                       /region_name="Conflict"
                       /note="D -> H (IN REF. 3)."
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Region 644

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                       /gene="VAS"
                       /region_name="Conflict"
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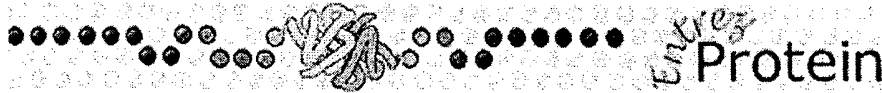
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121 frggeggrg rlyenedgde rrgrldreer ggerrgrldr eerggerger gdggfarrrr
181 neddinnnnn iaedverkre fyippepsnd aieifssgia sgihfskynn ipvkvtgsdv
241 pqpighftsa dlrddiidnv nksgfkiptp iqkcsipvis sgrdlmacaq tgsgktaafll
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661 d

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Features

BLink, Domains, Links

1: Q64060. DEAD-box protein ...[gi:2500526]

LOCUS Q64060 713 aa linear ROD 01-NOV-1997

DEFINITION DEAD BOX PROTEIN 4 (VASA HOMOLOG) (RVLG).

ACCESSION Q64060

VERSION Q64060 GI:2500526

DBSOURCE swissprot: locus DDX4_RAT, accession Q64060;

class: standard.

created: Nov 1, 1997.

sequence updated: Nov 1, 1997.

annotation updated: Nov 1, 1997.

xrefs: gi: 806463, gi: 806464

xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,

PROSITEPS00039

KEYWORDS ATP-binding; Helicase; RNA-binding.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (residues 1 to 713)

AUTHORS Komiya,T. and Tanigawa,Y.

TITLE Cloning of a gene of the DEAD box protein family which is specifically expressed in germ cells in rats

JOURNAL Biochem. Biophys. Res. Commun. 207 (1), 405-410 (1995)

MEDLINE 95160706

REMARK SEQUENCE FROM N.A.

STRAIN=WISTAR; TISSUE=TESTIS

COMMENT

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[TISSUE SPECIFICITY] TESTIS.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. HIGHEST TO DROSOPHILA VASA.

FEATURES

Location/Qualifiers

source

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/organism="Rattus norvegicus"

/db_xref="taxon:10116"

gene

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/gene="DDX4"

Protein

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/gene="DDX4"

/product="DEAD BOX PROTEIN 4"

Site

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/gene="DDX4"

/site_type="np-binding"

/note="ATP (POTENTIAL)."

Site

431..434

/gene="DDX4"

/site_type="unclassified"

/note="DEAD BOX."

ORIGIN

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121 dtqtrsrgfs krggypdgnd seasgpfrg grdseydqdg gsqrggglfg srkpaasdsg
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361 elinqiylea rkfsfgtcvr avviygggtqf ghsirqivqg cnilcatpgr lmdiigkeki
421 glkqvkyvl deadrmlmg fgpemkkkis cpgmpskeqr qtllfsatfp eeiqrlagef
481 lksnylfvav gqvvggacrdv qqsilqvgpv fkrklveil rnigderpmv fvetkkkadf
541 iatflcqeki sttsihgdre qrereqalgd frcgkcpvlv atsvaargld ienvqhvinf
601 nlpstideyv hrigrtgrcg ntgraisffd tesdnhlaqp lvkvlsdaqg dvpawleeia
661 fssyappsfs nstrgavfas fdtrknfggk ntlntagiss aqapnpvdde swd

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Features

1: Q61496[gi:2500525] This record was replaced or removed. See revision history for details.

LOCUS Q61496 637 aa linear ROD 01-NOV-1997

DEFINITION DEAD BOX PROTEIN 4 (VASA HOMOLOG) (MVH).

ACCESSION Q61496

VERSION Q61496 GI:2500525

DBSOURCE swissprot: locus DDX4_MOUSE, accession Q61496;

class: standard.

created: Nov 1, 1997.

sequence updated: Nov 1, 1997.

annotation updated: Nov 1, 1997.

xrefs: gi: 286074, gi: 286075

xrefs (non-sequence databases): MGI102670, PFAMPF00270,

PFAMPF00271, PROSITEPS00039

KEYWORDS ATP-binding; Helicase; RNA-binding.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (residues 1 to 637)

AUTHORS Fujiwara,Y., Komiya,T., Kawabata,H., Sato,M., Fujimoto,H.,

Furusawa,M. and Noce,T.

TITLE Isolation of a DEAD-family protein gene that encodes a murine homolog of Drosophila vasa and its specific expression in germ cell lineage

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (25), 12258-12262 (1994)

MEDLINE 95083681

REMARK SEQUENCE FROM N.A.

STRAIN=BALB/C; TISSUE=TESTIS

COMMENT

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[SUBCELLULAR LOCATION] CYTOPLASMIC AND PERINUCLEAR.

[TISSUE SPECIFICITY] TESTIS.

[DEVELOPMENTAL STAGE] EXPRESSED IN SPERMATOGENIC CELLS FROM THE SPERMATOCYTE STAGE TO THE ROUND SPERMATID STAGE.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. HIGHEST TO DROSOPHILA VASA.

FEATURES

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gene	1..637 /gene="DDX4" /note="synonym: MVH"
Protein	<1..637 /gene="DDX4" /product="DEAD BOX PROTEIN 4"
Site	246..253 /gene="DDX4"

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/note="ATP (BY SIMILARITY)."
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/gene="DDX4"
/site_type="unclassified"
/note="DEAD BOX."

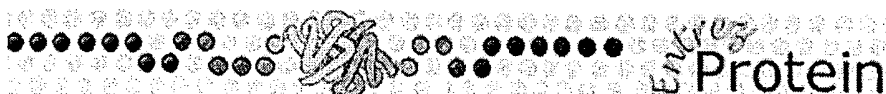
ORIGIN

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121 grggykglne evvtgsgkns wksetegges sdsqgpkvty ipppppeded sifahyqtgi
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241 dlmacagtgs gktaafllpi lahmrdgit asrfkelqep eciivaptre linqiylear
301 kfsfgtcvis vviygtqf ghsrvqivqgc nilcatpgrl mdiigkekig lkqvkvylvld
361 eadsmldmgf apeikkllsc pgmpskeqhq tllfsatfpe eiqlragdfl ksnylflvavg
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Features

1: Q62167. DEAD-box protein ...[gi:2500528]

BLink, Domains, Links

LOCUS Q62167 662 aa linear ROD 15-JUL-1999

DEFINITION DEAD BOX PROTEIN 3 (DEAD-BOX RNA HELICASE DEAD3) (MDEAD3)
(EMBRYONIC RNA HELICASE) (D1PAS1 RELATED SEQUENCE 2).

ACCESSION Q62167

VERSION Q62167 GI:2500528

DBSOURCE swissprot: locus DDX3_MOUSE, accession Q62167;
class: standard.

extra accessions:009060,009143,created: Nov 1, 1997.

sequence updated: Nov 1, 1997.

annotation updated: Jul 15, 1999.

xrefs: gi: 1835121, gi: 1835122, gi: 407995, gi: 407996

xrefs (non-sequence databases): MGI103064, PFAMPF00270,
PFAMPF00271, PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (residues 1 to 662)

AUTHORS Sowden,J., Putt,W., Morrison,K., Beddington,R. and Edwards,Y.

TITLE The embryonic RNA helicase gene (ERH): a new member of the DEAD box
family of RNA helicases

JOURNAL Biochem. J. 308 (Pt 3), 839-846 (1995)

MEDLINE 97104282

REMARK SEQUENCE FROM N.A.

STRAIN=C57BL/6, AND DBA

REFERENCE 2 (residues 1 to 662)

AUTHORS Gee,S.L. and Conboy,J.G.

TITLE Mouse erythroid cells express multiple putative RNA helicase genes
exhibiting high sequence conservation from yeast to mammals

JOURNAL Gene 140 (2), 171-177 (1994)

MEDLINE 94192995

REMARK SEQUENCE FROM N.A.

TISSUE=ERYTHROLEUKEMIA

COMMENT

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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.

The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. IT MAY PLAY A ROLE
IN TRANSLATIONAL ACTIVATION OF MRNA IN THE OOCYTE AND EARLY EMBRYO.

[TISSUE SPECIFICITY] DEVELOPMENTALLY REGULATED.

[DEVELOPMENTAL STAGE] EXPRESSED IN OOCYTES. UBIQUITOUSLY FOUND IN 9
DAYS POST-CONCEPTION EMBRYO, AT LATER STAGES IT IS RESTRICTED TO
BRAIN AND KIDNEY.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
PL10 SUBFAMILY.

FEATURES Location/Qualifiers

source 1..662

/organism="Mus musculus"

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/db_xref="taxon:10090"
gene      1..662
          /gene="DDX3"
          /note="synonyms: DEAD3, ERH, D1PAS1-RS2"
Protein   1..662
          /gene="DDX3"
          /product="DEAD BOX PROTEIN 3"
Site      224..231
          /gene="DDX3"
          /site_type="np-binding"
          /note="ATP (POTENTIAL).".
Site      347..350
          /gene="DDX3"
          /site_type="unclassified"
          /note="DEAD BOX."
Region    582..662
          /gene="DDX3"
          /region_name="Domain"
          /note="GLY/SER-RICH."
Region    609..616
          /gene="DDX3"
          /region_name="Domain"
          /note="POLY-SER."
Region    624..630
          /gene="DDX3"
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          /note="POLY-GLY."
Region    633..641
          /gene="DDX3"
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          /note="POLY-GLY."

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ORIGIN

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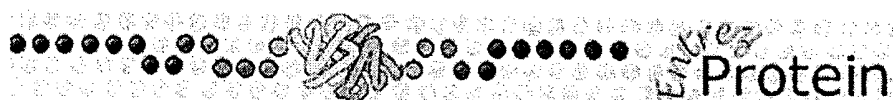
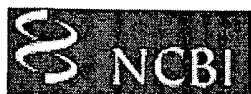
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181 sfsdvemgei imgnieltry trptpvqkha ipiikekrdl macaqtgsgk taafllpils
241 qiyadgpgea lramkengry grrkqypisl vlaptrelav qiyeearkfs yrsrvrpcvv
301 yggaeigqqi rdlergchll vatpgrlvdm mergkigldf ckylvldead rmldmgfepq
361 irriveqdtm ppkgvrhtmm fsatfpkeiq mlardfldey iflavgrvgs tsenitqkvv
421 wveeidkrsf lldllnatgk dsltlvfvvet kkgadsledf lyhegyacts ihgdrsqrdr
481 eealhqrfrsg kspilvatav aargldisnv khvinfdlps dieeyvhrig rtgrvgnlgl
541 atsffnerni nitkdllldll veakqevpsw lenmafehhy kgssrgrsks srfsggfgar
601 dyrqssgass ssfsssrass srsgggghgg srgfggggyg gfynsdgygg nynsqgvdww
661 gn

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Features

1: O00571. DEAD-box protein ...[gi:3023628]

BLink, Domains, Links

LOCUS O00571 662 aa linear PRI 15-JUL-1999
DEFINITION DEAD BOX PROTEIN 3 (HELICASE-LIKE PROTEIN 2) (HLP2) (DEAD BOX, X ISOFORM).

ACCESSION O00571
VERSION O00571 GI:3023628
DBSOURCE swissprot: locus DDX3_HUMAN, accession O00571;
class: standard.
extra accessions: O15536, created: Jul 15, 1998.
sequence updated: Jul 15, 1998.
annotation updated: Jul 15, 1999.

xrefs: gi: 2148923, gi: 2148924, gi: 3523149, gi: 3523150, gi: 2580551, gi: 2580552, gi: 2580549, gi: 2580550
xrefs (non-sequence databases): MIM 300160, PFAMPF00270, PFAMPF00271, PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 662)

AUTHORS CHUNG, J., LEE, S.-G. and SONG, K.

TITLE Identification of a human homolog of a putative RNA helicase gene (mDEAD3) expressed in mouse erythroid cells

JOURNAL Korean J. Biochem. 27, 193-197 (1995)

REMARK SEQUENCE FROM N.A.

TISSUE=LIVER, AND HIPPOCAMPUS

REFERENCE 2 (residues 1 to 662)

AUTHORS OWSIANKA, A.M. and PATEL, A.H.

TITLE Direct Submission

JOURNAL Submitted (~APR-1998)

REMARK SEQUENCE FROM N.A.

REFERENCE 3 (residues 1 to 662)

AUTHORS Lahn, B.T. and Page, D.C.

TITLE Functional coherence of the human Y chromosome

JOURNAL Science 278 (5338), 675-680 (1997)

MEDLINE 98022381

REMARK SEQUENCE FROM N.A.

COMMENT

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[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. INTERACTS SPECIFICALLY WITH HEPATITIS C VIRUS CORE PROTEIN RESULTING A CHANGE IN INTRACELLULAR LOCATION.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE PL10 SUBFAMILY.

FEATURES Location/Qualifiers
source 1..662
/organism="Homo sapiens"

/db_xref="taxon:9606"
gene 1..662
 /gene="DDX3"
 /note="synonym: DBX"
Protein 1..662
 /gene="DDX3"
 /product="DEAD BOX PROTEIN 3"
Region 50
 /gene="DDX3"
 /region_name="Conflict"
 /note="K -> R (IN REF. 3)."
Site 224..231
 /gene="DDX3"
 /site_type="np-binding"
 /note="ATP (POTENTIAL)."
Site 347..350
 /gene="DDX3"
 /site_type="unclassified"
 /note="DEAD BOX."
Region 582..662
 /gene="DDX3"
 /region_name="Domain"
 /note="GLY/SER-RICH."

ORIGIN
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 61 ssskdkdays sfgsrdsrg kssffsdrqs gsrgrfddrg rsdydgigsr gdrsgfgkfe
 121 rggnsrwcdk sdeddwsapl ppserleqel fsggntginf ekyddipvea tgnncpphie
 181 sfsdvemgei imgnieltry trptpvqkha ipiikekrdl macagtgsrk taafllpils
 241 qiysdgpgea lramkengry grrkqypisl vlaptrelav qiyeearkfs yrsrvrvcvv
 301 yggadigqqi rdlergchll vatpgrlvdn mergkigldf ckylvldead rmldmgfepq
 361 irriveqdtm ppgkvrhtmm fsatfpkeiq mlardflday iflavgrvgs tsenitqkvv
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 481 eealhqrfrg kspilvatav aargldisn khvinfdlps dieeyvhrig rtgrvgnlgl
 541 atsffnorni nitkdllldl veakqevpsw lenmayehhy kgssrgrsks srfsggfgar
 601 dyrqssgass ssfsssrass srsgggghgs srgfggggyg gfynsdgygg nysqgvdww
 661 gn

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1: P24346. Putative ATP-depe...[gi:113825] BLink, Domains, Links

LOCUS P24346 697 aa linear VRT 01-FEB-1996

DEFINITION PUTATIVE ATP-DEPENDENT RNA HELICASE AN3.

ACCESSION P24346

VERSION P24346 GI:113825

DBSOURCE swissprot: locus AN3_XENLA, accession P24346;
class: standard.
created: Mar 1, 1992.
sequence updated: Mar 1, 1992.
annotation updated: Feb 1, 1996.
xrefs: gi: 65059, gi: 65060, gi: 103989, gi: 345587
xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,
PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
Xenopus.

REFERENCE 1 (residues 1 to 697)

AUTHORS Gururajan,R., Perry-O'Keefe,H., Melton,D.A. and Weeks,D.L.

TITLE The Xenopus localized messenger RNA An3 may encode an ATP-dependent
RNA helicase

JOURNAL Nature 349 (6311), 717-719 (1991)

MEDLINE 91141586

REMARK SEQUENCE FROM N.A.

COMMENT

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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
PL10 SUBFAMILY.

FEATURES Location/Qualifiers

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/db_xref="taxon:8355"
gene 1..697
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Protein 1..697
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Site 388..391
/gene="AN3"
/site_type="unclassified"
/note="DEAD BOX."

Region

623..697

/gene="AN3"

/region_name="Domain"

/note="GLY/SER-RICH."

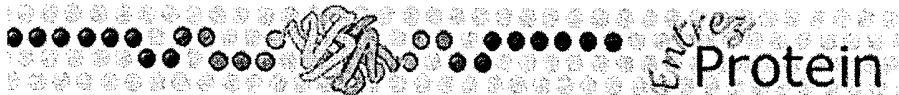
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121 rgkgslnfner gsgsrtrddr rqdqfdgmgn rsdksgfgrf drgnsrwsdd rndeddwskp
181 lapndrveqe lfsgsntgin fekyddipve atgsncpphi esfhdtmge iimgniqltr
241 ytrptpvqkh aipiiiekrd lmacaqtgsg ktaafllpil sqiyadgpgd amkhlqengr
301 ygrrkqfpls lvlaptrela vqiyeearkf ayrsrvrvcv vyggadigqq irdlergchl
361 lvatpgrlvd mmergkigld fckylvldea drmlmngfep qirriveqdt mppkgvrqtm
421 mfsatfpkei qilardflde yiiflavgrvg stsenitqkv vwveemdkrs flldllnatg
481 kdsltlvfve tkkgadaled flyhegyact sihgdrsqrd reealhqrfs gkspilvata
541 vaargldisn vkhvinfdlp sdieeyvhri grtgrvgnlg latsffnekn initkdllldl
601 lveakqevps wlenmayeqh hksssrgrsk srfsggfgak dyrqssgags sfgssrggrs
661 sghggsrgfg ggyggfynd gyggyggss qvdwwgn
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Display default Show: 20 Send to File Get Subsequence Features

1: P16381. Putative ATP-depe...[gi:130256]

BLink, Domains, Links

LOCUS P16381 660 aa linear ROD 15-JUL-1999

DEFINITION PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.

ACCESSION P16381

VERSION P16381 GI:130256

DBSOURCE swissprot: locus PL10_MOUSE, accession P16381;
class: standard.
created: Aug 1, 1990.
sequence updated: Aug 1, 1990.
annotation updated: Jul 15, 1999.
xrefs: gi: 200388, gi: 200389, gi: 110038
xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,
PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding; Spermatogenesis.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (residues 1 to 660)

AUTHORS Leroy,P., Alzari,P., Sassoon,D., Wolgemuth,D. and Fellous,M.

TITLE The protein encoded by a murine male germ cell-specific transcript
is a putative ATP-dependent RNA helicase

JOURNAL Cell 57 (4), 549-559 (1989)

MEDLINE 89249320

REMARK SEQUENCE FROM N.A.
TISSUE=TESTIS

COMMENT -----
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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. POSSIBLE ROLE IN A
KEY STEP OF THE SPERMATOGENIC PROCESS.
[TISSUE SPECIFICITY] TESTIS.
[DEVELOPMENTAL STAGE] HIGH LEVELS OF PL10 DURING THE MEIOTIC AND
HAPLOID STAGES OF SPERMATOGENESIS.
[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
PL10 SUBFAMILY.

FEATURES Location/Qualifiers

source 1..660
/organism="Mus musculus"
/db_xref="taxon:10090"

gene 1..660
/gene="PL10"
/note="synonym: D1PAS1"

Protein 1..660
/gene="PL10"
/product="PUTATIVE ATP-DEPENDENT RNA HELICASE PL10"

Site 223..230
/gene="PL10"
/site_type="np-binding"

Site /note="ATP (POTENTIAL)."
 346..349
 /gene="PL10"
 /site_type="unclassified"
Site /note="DEAD BOX."
 495..514
 /gene="PL10"
 /site_type="DNA binding"
Region /note="POTENTIAL."
 581..660
 /gene="PL10"
 /region_name="Domain"
 /note="GLY/SER-RICH."

ORIGIN

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121 ggnsrwcdka deddwscklp pserleqelf sggntginfe kyddipveat gnnpphies
181 fsdvemgeii mgnieltryt rtpvqkhai piikekrdm acaqtgsgkt aafllpilsq
241 iytdgpgeal ramkengkyg rrkqypisl lvaptrelavq iyeearkfsy rsvrvcvvy
301 ggadigqqir dlergchllv atpgrlvdmn ergkigldfc kylvldeadr mldmgfepqi
361 rriveqdtmp pkgvrhtmmf satfpkeiqm lardfldeyi flavgrvgst senitqkvvw
421 veeadkrsfl ldllnatgkd slilvfvetk kgadsledfl yhegyactsi hgdrsqrdre
481 ealhqfrsgk spilvatava argldisnvk hvinfldpsd ieeyvhrigr tgrvgnlgla
541 tsffnernin itkdlldllv eakqevpswl enmafehhyk ggsrgrsksr fsggfgardy
601 rqssgassss fssgrasnsr sgggshgssr gfgggsyggf ynsdgyggny ssqgvdwgn
  
```

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Features

1: O15523. DEAD-box protein ...[gi:6014945]

BLink, Domains, Links

LOCUS O15523 660 aa linear PRI 15-JUL-1999

DEFINITION DEAD BOX PROTEIN 3, Y-CHROMOSOMAL.

ACCESSION O15523

VERSION O15523 GI:6014945

DBSOURCE swissprot: locus DDX_Y_HUMAN, accession O15523;

class: standard.

created: Jul 15, 1999.

sequence updated: Jul 15, 1999.

annotation updated: Jul 15, 1999.

xrefs: gi: 2580555, gi: 2580556, gi: 2580553, gi: 2580554

xrefs (non-sequence databases): MIM 400010, PFAMPF00270,

PFAMPF00271, PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 660)

AUTHORS Lahn,B.T. and Page,D.C.

TITLE Functional coherence of the human Y chromosome

JOURNAL Science 278 (5338), 675-680 (1997)

MEDLINE 98022381

REMARK SEQUENCE FROM N.A.

COMMENT

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[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE PL10 SUBFAMILY.

FEATURES Location/Qualifiers

source 1..660
/organism="Homo sapiens"
/db_xref="taxon:9606"

gene 1..660
/gene="DBY"

Protein 1..660
/gene="DBY"
/product="DEAD BOX PROTEIN 3, Y-CHROMOSOMAL"

Site 222..229
/gene="DBY"
/site_type="np-binding"
/note="ATP (POTENTIAL)."

Site 345..348
/gene="DBY"
/site_type="unclassified"
/note="DEAD BOX."

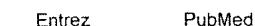
ORIGIN

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61 scskdkdays sfgsrdsrgk pgyfsergsg srgrfddrgr sdydgignre rpgfgrfers

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121 ghsrwcdksv eddwskplpp serleqelfs ggntginfek yddipveatg sncpphienf
181 sdidmgeiim gnieltrytr ptpvqkhaip iikgkrdlva caqtgsgkta afllpilsqi
241 ytdgpgealk avkengrygr rkqypislvl aptrelavqi yeearkfsyr srvrpcvvyg
301 gadigqqird lergchllva tpgrlvdmm rkgigldfck ylvldeadrm ldmgfpqir
361 riveqdtmpp kgvrhtmmfs atfpkeiqml ardfldeyif lavgrvgsts enitqkvvvw
421 edldkrsfll dilgatgds ltlvfvetkk gadsledfly hegyactsih gdrsqrdrree
481 alhqfrsgks pilvatavaa rgldisnvrh vinfdlpsdi eeyvhrigrt grvgnlglat
541 sffneknmni tkdlldllve akqevpswle nmayehhykg gsrgrsksnr fsggfgardy
601 rqssgssssg fgasrgssr sgggygdsr gfggggyggf ynsdgyggny nsqgvdwgn

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1: AL042306. DKFZp434M0720 r1 ...[gi:5421648]

Links

[IDENTIFIERS]

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1bEST Id:          2890414
EST name:          DKFZp434M0720_r1
3enBank Acc:       AL042306
3enBank gi:        5421648
Database:          RZPD      Cross Reference:      DKFZp434M0720

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CLONE INFO

Clone Id: DKFZp434M0720 (5')
DNA type: cDNA

PRIMERS

PolyA Tail: Unknown

SEQUENCE

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CTTCTATGTTCCCATATTTGAGAAGGATAGGTATTCTGGAGAAAATGGAGACAATTTTA
ACAGGACTCCAGCTTCATCATCAGAAATGGATGATGGACCTTCTCGAAGAGATCATTTC
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ATGGAAATAATTAGAAGCTTCAGGGCCATACAGAGAGGTGGAGAGGTAGTTTTCCGAGG
TG

Entry Created: Jul 8 1999
Last Updated: Sep 4 2003

COMMENTS

This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German
Cancer Research Center (DKFZ); Email [s.wiemann@dkfz-
heidelberg.de](mailto:s.wiemann@dkfz-heidelberg.de); sequenced by MediGenomix (Martinsried/Germany
) within the cDNA sequencing consortium of the German Genome
Project. No sl sequence available.
This clone (DKFZp434M0720) is available at the RZPD in
Berlin. Please contact the RZPD: Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email:
clone@rzpd.de

LIBRARY

Lib Name: 434 (synonym: htes3)
Organism: Homo sapiens
Tissue type: testis
Develop. stage: adult
Lab host: DH10B
Vector: pSport1
R. Site 1: NotI
R. Site 2: SalI

SUBMITTER

Name: MIPS
Institution: MIPS
Address: Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

CITATIONS

Title: EST (Ottenwaelder, et al.)
Authors: Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J.,
Wiemann,S.
Year: 1999
Status: Unpublished

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Check sequence revision history

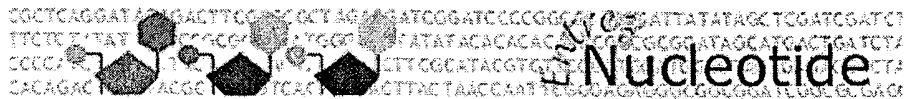
How to create WWW links to Entrez

[LinkOut](#)[Cubby](#)[Related resources](#)[BLAST](#)[Reference sequence project](#)[LocusLink](#)[Clusters of orthologous groups](#)[Protein reviews on the web](#)

GI	Version	Update Date	Status
5421648	1	Jul 8 1999 7:06 PM	Live

Accession AL042306 was first seen at NCBI on Jul 8 1999 7:06 PM

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Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo

(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library went
through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-Merck EST Project 1997
Authors: Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost
, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising
, B., White, Y., Wylie, T., Waterston, R., Wilson, R.
Year: 1997
Status: Unpublished

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5' Nucleotide

CCCTCAGGATATGACTTCCGCTCCTAGATCGGATCCCGGCTTCTATTATATACTCGATCGATCT
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 CCCCCT
 CACACACCTACCGCTTCT

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1: AA398976.zt93a07.r1 Soares...[gi:2052713]

Links

IDENTIFIERS

Best Id: 1040482
 EST name: zt93a07.r1
 GenBank Acc: AA398976
 GenBank gi: 2052713
 EDB Id: 5926405

CLONE INFO

Clone Id: IMAGE:729876 (5')
 Source: IMAGE Consortium, LLNL
 DNA type: cDNA

PRIMERS

Sequencing: -28ml3 rev2 ET from Amersham
 PolyA Tail: Unknown

SEQUENCE

ATTGATGAATATGTTTCATCGAATTGGGCGTACTGGTCGTTGTGGGAATACTGGCAGACAA
 TTTCCTTTTTTGATCTTGAATCGGATAACCATTTAGCACAGCCTCTAGTAAAAGTATTGA
 CAGATGCTCAACAGGATGTTCTGCATGGTTGGAAGAAATTGCCTTTAGTACATACATTC
 CTGGCTTCAGTGGTAGTACAAGAGGAAACGTGTTTCATCAGTTGATACCAGAAAGGGCA
 AGAGCACTTTGAACACAGCTGGGTTTTCTTCTCACAAGCTCCCAATCCAGTAGATGATG
 AGTCATGGGATTAAAGCCAAAACATCCTTCAAGTCTGTGGTTTTGATGCAGAGAAGAAAA
 TAGTTTTGATTTTTGAGTTTTTAACAGAAGTATAAACTTAACATTCTCATAGCTCCTGT
 CCTTGTATTCTCACTCCTACACTTAAAAAAAATCCTTACTGACTAGTTATGTGAGATG
 CTAAAACTTAC

Entry Created: Apr 28 1997
 Last Updated: May 16 1997

COMMENTS

This clone is available royalty-free through LLNL ; contact
 the IMAGE Consortium (info@image.llnl.gov) for further
 information.
 Putative full length read
 The vector to vector length is 554

PUTATIVE ID Assigned by submitter
 TR:G286075 G286075 DROSOPHILA VASA HOMOLOGUE ;

LIBRARY

Lib Name: Soares_testis_NHT
 Organism: Homo sapiens
 Sex: male
 Lab host: DH10B
 Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
 R. Site 1: Not I
 R. Site 2: Eco RI
 Description: 1st strand cDNA was prepared from mRNA obtained from
 Clontech Laboratories, Inc., and primed with a Not I - oligo
 (dT) primer [5'

TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library went
through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-Merck EST Project 1997
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost
,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising
,B., White,Y., Wylie,T., Waterston,R., Wilson,R.
Year: 1997
Status: Unpublished

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CCGTCAGGATAGGACTTCGCGGCTAGGATCGGATCCCGGCGGATATTATATAGCTGGATCGATCT
 TTCCTATATATGCGGATGCGGATATATACACACACAGCTGCGGATAGGATGATGATCT
 CCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT
 CACAGACTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT

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1: AA383535. EST96928 Testis I...[gi:2035852]

Links

IDENTIFIERS

EST Id: 1024841
 EST name: EST96928
 GenBank Acc: AA383535
 GenBank gi: 2035852

CLONE INFO

Clone Id: (5' end)
 Source: ATCC
 Id in host: 187704
 DNA type: cDNA

PRIMERS

Sequencing: M13 Reverse
 PolyA Tail: Unknown

SEQUENCE

TTATATATGGGGGAACCCAGCTGGGACATTCAATTCGACAAATAGTACAAGGCTGTAATA
 TATATATGTGCTACTCCTGGAAGACTGATGGATATCATAGGCAAAGAAAAGATTGGTCTCA
 AACAGATCAAATACTTAGTTTTGGATGAAGCTGATCGCATGTTGGATATGGGTTTTGGTC
 CAGAAATGAAGAAGTTAATTNNNTGCCAGGAATGCCATCAAAGGAACAGCGCCAAACCC
 TTATGTTCACTGCAACTTTTCCAGAGGAAATTCAAAGGTTGGCTGCAGAGTTTTTAAAGT
 CAAATTATCTGTTTGTGCTGTTGGACAAGTGGGT

Entry Created: Apr 21 1997
 Last Updated: Apr 21 1997

COMMENTS

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

PUTATIVE ID Assigned by submitter
 similar to vasa homolog

LIBRARY

Lib Name: Testis I
 Organism: Homo sapiens
 Sex: male
 Organ: testis
 Develop. stage: adult
 Vector: pBluescript SK-
 R. Site 1: EcoRI
 R. Site 2: XhoI

SUBMITTER

Name: Kerlavage, AR
 Lab: Bioinformatics
 Institution: The Institute for Genomic Research
 Address: 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056

Fax: 3018699423
E-mail: arkerlav@tigr.org

CITATIONS

Medline UID: [96026280](#)

Title: Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Authors: Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., Venter,J.C.

Citation: Nature 377 (6547 Suppl): 3-174 1995

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ORIGIN

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121 ccgctcagac tggagtcttc atgctgagta gagcgggtgtg tgaacacttg aggcctgcag
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3001 aacacatttc cccctaaaaa aaaaaaaaaa
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File

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Featu

1: D14859. Mus musculus mRNA...[gi:286074]

Links

LOCUS	MUSDVH	1930 bp	mRNA	linear	ROD 04-FEB-1999
DEFINITION	Mouse mRNA for drosophila vasa homologue, partial cds.				
ACCESSION	D14859				
VERSION	D14859.1 GI:286074				
KEYWORDS	RNA helicase; drosophila vasa homologue.				
SOURCE	Mus musculus				
ORGANISM	<u>Mus musculus</u> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1930)				
AUTHORS	Noce,T.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-APR-1993) Toshiaki Noce, Mitsubishi Kasei Institute of Life Sciences, Developmental Biology; 11 Minamiooya, Machida, Tokyo 194, Japan (Tel:0427-24-6246, Fax:0427-29-1252)				
REFERENCE	2 (bases 1 to 1930)				
AUTHORS	Noce,T.				
JOURNAL	Unpublished (1994)				
REFERENCE	3 (sites)				
AUTHORS	Fujiwara,Y., Komiya,T., Kawabata,H., Sato,M., Fujimoto,H., Furusawa,M. and Noce,T.				
TITLE	Isolation of a DEAD-family protein gene that encodes a murine homolog of Drosophila vasa and its specific expression in germ cell lineage				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (25), 12258-12262 (1994)				
MEDLINE	<u>95083681</u>				
PUBMED	7991615				

FEATURES	Location/Qualifiers
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<u>CDS</u>	<1..1914 /function="RNA helicase" /codon_start=1 /product="Drosophila vasa homologue" /protein_id=" <u>BAA03584.1</u> " /db_xref="GI:286075" /translation="FGRGKGFGNRGFLNNKFEEDSSGFWKESNNDCEDNQTRSRGFS KRGGCQDGNDSASGPFRRGGRGSFRGCRGGFGLGRPNSESDQDQGTQCGGGFLVLGK PAASDSGNGDITYQSRSGSGRGGYKGLNEEVVVTGSGKNSWKSETEGGESDSSQGPKVTY IPPPPPEDEDSIFAHYQTGINFDKYDTILVEVSGHDAPPAILTFEEANLCOTLNNNI



5' Nucleotide

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☐ 1: AI217144.qf47d11.x1 Soares...[gi:3796959] Links

IDENTIFIERS

dbEST Id: 1988110
EST name: qf47d11.x1
GenBank Acc: AI217144
GenBank gi: 3796959

CLONE INFO

Clone Id: IMAGE:1753173 (3')
Source: NCI
Insert length: 1013
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

TTTTTTTTTTTTTTTTTTTTTTTTTTTGACATTTAAAATGCTTTAATATTCCCAGTTAACACC
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TTCCAACCATGCAGGAACATCCTGTTGAGCATCTGTCAATACTTTTACTAGAGGCTGTGC
TAAATGGTTATCCGATTCAAGATCAAAAAAGGAAATTGCTCTGCCAGTATTCCCACAACG
ACCAGNACGCCCAAT

Quality: High quality sequence stops at base: 448

Entry Created: Oct 26 1998
Last Updated: Nov 10 1998

COMMENTS

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name: Soares_testis_NHT
Organism: Homo sapiens
Sex: male
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker

\. Site 1: Not I
\. Site 2: Eco RI
Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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CGCTCAGGATTCGACTTCGATCGTAGAGGATCGGATCCCGGCGCTGATATATATAGCTCGATCGATCT
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CCCGGATTCGACTTCGATCGTAGAGGATCGGATCCCGGCGCTGATATATATAGCTCGATCGATCT
CACAGACTTCGACTTCGATCGTAGAGGATCGGATCCCGGCGCTGATATATATAGCTCGATCGATCT

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1: A1953070. wq49h07.x1 NCI_CG...[gi:5745380]

Links

IDENTIFIERS

dbEST Id: 3076455
EST name: wq49h07.x1
GenBank Acc: A1953070
GenBank gi: 5745380

CLONE INFO

Clone Id: IMAGE:2474653 (3')
Source: NCI
Insert length: 450
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

TTTTTTTTTTATGAGAATGTTAAGTTTTTATACTTCTGTAAAAAACTCAAAAATCAAAACT
ATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGATGTTTGGCTTTAATCCCATGAC
TCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAAACCCAGCTGTGTTCAAAGTGCTC
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GGAATGTATGTACTAAAGGCAATTTCTTCCAACCATGCAGGAACATCCTGTTGAGCATCT
GTCAATACTTTTACTAGAGGCTGTGCTAAATGGTTATCCGATTCAAG

Entry Created: Aug 19 1999
Last Updated: Mar 8 2000

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name: NCI_CGAP_GC6
Organism: Homo sapiens
Tissue type: pooled germ cell tumors
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Plasmid DNA from the normalized library NCI_CGAP_GC4 was

prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

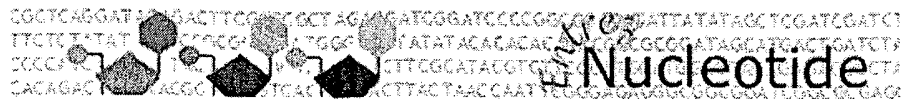
CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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1: AI025074. ov40a04.x1 Soares...[gi:3240687]

Links

IDENTIFIERS

dbEST Id: 1764280
EST name: ov40a04.x1
GenBank Acc: AI025074
GenBank gi: 3240687

CLONE INFO

Clone Id: IMAGE:1639758 (3')
Source: NCI
Insert length: 587
DNA type: cDNA

PRIMERS

Sequencing: -40m13 fwd. ET from Amersham
PolyA Tail: Unknown

SEQUENCE

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TGTTGAGCATCTGTCAATACTTTACTAGAAGCTGTGCTAAATGGTTATC

Quality: High quality sequence stops at base: 408

Entry Created: Aug 13 1998
Last Updated: Aug 27 1998

COMMENTS

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4 RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

```

Lib Name:      Soares_testis_NHT
Organism:      Homo sapiens
Sex:           male
Lab host:      DH10B
Vector:        pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:     Not I
R. Site 2:     Eco RI

```

Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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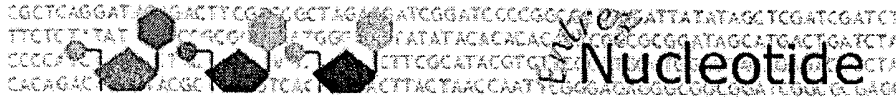
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GI	Version	Update Date	Status
5745380	1	Aug 19 1999 7:22 PM	Live

Accession AI953070 was first seen at NCBI on Aug 19 1999 7:22 PM

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dbEST Id: 2483061
EST name: wb31f04.x1
GenBank Acc: AI654417
GenBank gi: 4738396

Clone Id: IMAGE:2307295 (3')
Source: NCI
Insert length: 376
DNA type: cDNA

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

AAGTGTAGGTTTTGAGAATACAAGGACAGGAGCTATGAGAATGTTAAGTTTTTATACTTCTG
TTAAAAACTCAAAATCAAACTATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGA
TGTTTTTGCTTTTAATCCCATGACTCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAA
ACCCAGCTGTGTTCAAAGTGCTCTTGCCCTTCTGGTATCAACTGATGCAAAACAGTTTTCT
CTCTTGTA CTACTACCACTGAAGCCAGGAATGTATGTACTAAAGGCAATTTCTTCCAACCATG

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

LIBRARY

```

Lib Name:      NCI_CGAP_GC6
Organism:      Homo sapiens
Tissue type:   pooled germ cell tumors
Lab host:      DH10B
Vector:        pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:     Not I
R. Site 2:     Eco RI
Description:    Plasmid DNA from the normalized library NCI_CGAP_GC4 was
                prepared, and ss circles were made in vitro. Following HAP

```

purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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Revision history for AI654417

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information for human, fruit
fly, mouse, rat, and
zebrafish

GI	Version	Update Date	Status
4738396	1	May 4 1999 7:20 PM	Live

Accession AI654417 was first seen at NCBI on May 4 1999 7:20 PM

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CGCTCAGGATTTGACTTCCTGCTAGAGATCGGATCCCGGCGCTATTATATAGCTCGATCGATCT
TTCTCTATATCTCCGCTATGCGCTATATACACACACACCTCCCGCATAGCATGACTGATCTT
CCCGATCT
CACAGACTTACGCT

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1: AI337133.qx83b04.x1 NCI_CG...[gi:4074060]

Links

IDENTIFIERS

dbEST Id: 2120875
EST name: qx83b04.x1
GenBank Acc: AI337133
GenBank gi: 4074060

CLONE INFO

Clone Id: IMAGE:2009071 (3')
Source: NCI
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

AAGTGTAGGAGTGAGAATACAAGGACAGGAGCTATGAGAATGTTAAGTTTATACTTCTG
TAAAAAACTCAAAAATCAAACTATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGA
TGTTTTGGCTTTAATCCCATGACTCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAA
ACCCAGCTGTGTTCAAAGTGCTCTTGCCCTTTCTGGTATCAACTGATGCAAACACGTTTC
CTCTTGTACTIONACTGAAGCCAGGAATGTATGTACTAAAGGCAATTTCTTCCAACCATG

Entry Created: Dec 29 1998
Last Updated: Dec 29 1998

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonardo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name: NCI_CGAP_GC6
Organism: Homo sapiens
Tissue type: pooled germ cell tumors
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Plasmid DNA from the normalized library NCI_CGAP_GC4 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

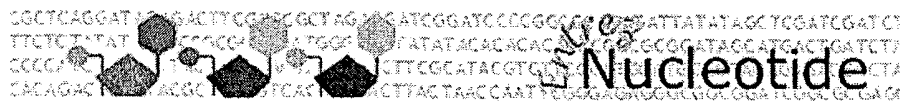
CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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1: AA758412. ah66g05.s1 Soares...[gi:2806275]

Links

IDENTIFIERS

dbEST Id: 1480155
EST name: ah66g05.s1
GenBank Acc: AA758412
GenBank qi: 2806275

CLONE INFO

Clone Id: 1320632 (3')
Source: IMAGE Consortium, LLNL
Insert length: 416
DNA type: cDNA

PRIMERS

Sequencing: -40ml3 fwd. ET from Amersham
PolyA Tail: Unknown

SEQUENCE

TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCATTTAGAATGCTTTAATATTCCCAG
TTAACACCATTGTATCAGTAACTGCAATGTTGTAAGTTTTAGCATCTCACATAACTAGI
CAGTAAGGATTTTTTTTTTAAAGTGTAGGAGTGAGAATACAAGGACAGGAGCTATGAGAAT
GTTAAGTTTTATACTTCTGTTAAAAACTCAAAAATCAAAACTATTTTCTTCTCTGCATCA
AAACCACAGACTTGAAGGATGTTTTGGCTTTAATCCCATGACTCATCATCTACTGGATTG
GGAGCTTGTGAAGAAGAAAACCCAGCTGTGTTCAAGAAGTGCTCTTGCCCTTTCTGGTATCA
ACTGATGCTCAA

Quality: High quality sequence stops at base: 206

Entry Created: Jan 23 1998
Last Updated: Dec 29 1998

COMMENTS

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cdNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand

PUTATIVE ID Assigned by submitter
SW:DDX4 RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

```

Lib Name:      Soares_testis_NHT
Organism:      Homo sapiens
Sex:           male
Lab host:      DH10B
Vector:        pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:     Not I
R. Site 2:     Eco RI

```

Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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1: AI969018. wq68d02.x1 NCI CG...[gi:5765757]

Links

IDENTIFIERS

dbEST Id: 3095021
EST name: wq68d02.x1
GenBank Acc: AI969018
GenBank qi: 5765757

CLONE INFO

Clone Id: IMAGE:2476419 (3')
Source: NCI
Insert length: 429
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

GAATGTATGTACTAAAGGCAATTTCTTCCAACCATGCAGGAACATCCTGTTGAGCATCTG
TCAATACTTTTACTAGAGGCTGTGCTAAATGGTTATCCGATTCAAGAT

Quality: Trace considered overall poor quality.

Entry Created: Aug 25 1999
Last Updated: Oct 20 2000

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality

Trace considered overall poor quality

PUTATIVE ID Assigned by submitter
SW:DDX4 RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name: NCI_CGAP_GC6
Organism: Homo sapiens
Tissue type: pooled germ cell tumors
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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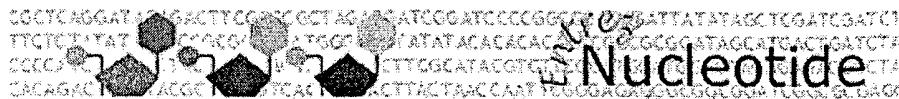
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GI	Version	Update Date	Status
5765757	1	Aug 25 1999 7:04 PM	Live

Accession AI969018 was first seen at NCBI on Aug 25 1999 7:04 PM

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	Display	default
Number of rows	10	10
Number of columns	80	80
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Background color	black	black
Text color	white	white
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Cursor shape	block	block
Cursor blink	no	yes
Scrolling	relative	relative
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Keyboard shortcuts	no	yes
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Font		

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 1: AA400066. zu62a08.s1 Soares...[gi:2053869]

Links

IDENTIFIERS

```
tbEST Id:      1041638
EST name:      zu62a08.s1
GenBank Acc:   AA400066
GenBank gi:    2053869
GDB Id:        5929433
```

CLONE INFO

Clone Id: IMAGE:742550 (3')
Source: IMAGE Consortium, LLNL
Insert length: 521
DNA type: cDNA

PRIMERS

Sequencing: -41m13 fwd. ET from Amersham
PolyA Tail: Unknown

SEQUENCE

GAATGTATGTACTATAGGCAATTTCTTCCATCCATGTCGGAACATCCTGTTGAGCATCTG
TCAATACTTTTACTAGAGGCTGTGCTACATGGCTAACCGAATC

Quality: Trace considered overall poor quality.

Entry Created: Dec 20 1996
Last Updated: Nov 9 1997

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

PUTATIVE ID Assigned by submitter
TR:G806464 G806464 VASA-LIKE GENE PROTEIN. ;

LIBRARY

```

Lib Name:      Soares_testis_NHT
Organism:      Homo sapiens
Sex:           male
Lab host:      DH10B
Vector:        pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:     Not I
R. Site 2:     Eco RI
Description:    1st strand cDNA was prepared from mRNA obtained from
                Clontech Laboratories, Inc., and primed with a Not I - oligo
                (dT) primer [5'
                TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTTT 3'].
                Double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. Library went
                through one round of normalization to Cot5, and was
                constructed by Bento Soares and M. Fatima Bonaldo.

```

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-NCI human EST Project
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost
,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra
,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan
,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson
,R.
Year: 1997
Status: Unpublished

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CGCTCAGGATAGGAGCTTCCTCCCTAGTGGATCCCGGGCTGATTATATAGCTCGATCGATCT
TTCTCTATATCTCCGCTTGTGGCTATATACACACACCTCCGCGATAGCAGTACTGATCT
CCCCACCT
CACAGACTTACGCTTCTCACT

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1: AA862553. oh44b08.s1 NCI_CG...[gi:2955032]

Links

IDENTIFIERS

dbEST Id: 1588408
EST name: oh44b08.s1
GenBank Acc: AA862553
GenBank gi: 2955032

CLONE INFO

Clone Id: IMAGE:1469463 (3')
Source: NCI
Insert length: 1202
DNA type: cDNA

PRIMERS

Sequencing: -40m13 fwd. ET from Amersham
PolyA Tail: Unknown

SEQUENCE

GAATGTATGTACTAAAGGCAATTTCTTCCAACCATGCAGTGACATCATGTTGAGCATCTG
TCAATACTTTTACTAGATGCTGTCTATAATAGGTATCGGA

Quality: Trace considered overall poor quality.

Entry Created: Mar 4 1998
Last Updated: Aug 24 1998

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name: NCI_CGAP_GC4
Organism: Homo sapiens
Tissue type: pooled germ cell tumors
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
Description: 1st strand cDNA was prepared from 3 pooled germ cell tumors,
and was then primed with a Not I - oligo(dT) primer.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library is
normalized. Library was constructed by Bento Soares and M.

Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project
(CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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CCCTCAGGATACGACTTCCTCCCTAGAGGATCGGATCCCCGCGATGATTATATAGCTCGATCGATC
TTCTCTATATATACCTACCTACCTGGATATATACACACACACCTCCGCGATAGCATGACTGATCT
CCCGATCT
CACAGACACCTACCT

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☐ 1: AA401568, zu62a08.r1 Soares...[gi:2053983]

Links

IDENTIFIERS

dbEST Id: 1041752
EST name: zu62a08.r1
GenBank Acc: AA401568
GenBank gi: 2053983
GDB Id: 5929433

CLONE INFO

Clone Id: IMAGE:742550 (5')
Source: IMAGE Consortium, LLNL
Insert length: 521
DNA type: cDNA

PRIMERS

Sequencing: -28m13 rev2 ET from Amersham
PolyA Tail: Unknown

SEQUENCE

TTCTACCATTGATGAATATGTTTCATCGACTTGGGCGTACTGGTCGTTGTGGGAATACTGG
CAGAGCAAGTTTCCTTTTT

Quality: Trace considered overall poor quality.

Entry Created: Dec 20 1996
Last Updated: Nov 9 1997

COMMENTS

This clone is available royalty-free through LLNL ; contact
the IMAGE Consortium (info@image.llnl.gov) for further
information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand

PUTATIVE ID Assigned by submitter
TR:G286075 G286075 DROSOPHILA VASA HOMOLOGUE ;

LIBRARY

Lib Name: Soares_testis_NHT
Organism: Homo sapiens
Sex: male
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: 1st strand cDNA was prepared from mRNA obtained from
Clontech Laboratories, Inc., and primed with a Not I - oligo
(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library went
through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
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Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-NCI human EST Project
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost
,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra
,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan
,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson
,R.
Year: 1997
Status: Unpublished

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5' **Nucleotide** 3'

45

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File

1: AA316798. EST188483 HCC cel...[gi:1969147]

Links

IDENTIFIERS

dbEST Id: 958127
EST name: EST188483
GenBank Acc: AA316798
GenBank gi: 1969147

CLONE INFO

Clone Id: (5' end)
Source: ATCC
Id in host: 113555
Other ESTs on clone: THC127206
DNA type: cDNA

PRIMERS

Sequencing: M13 Reverse
PolyA Tail: Unknown

SEQUENCE

GAAAGATTGGATTAGACTTTTGC AAATACTTGGTGT TAGATGAAGCTGATCGGATGTTGG
ATATGGGGTTTGGAGCCTCAGATTTCGTAG AATAGTCGAACAAGATACTATGCCTCCAAAGG
GTGTCCGCCACACTATGATGTTTAGTGCTACTTTTCCTAAGGAAATACAGATGCTGGCTC
GTGATTTCTTAGATGAATATATCTTCTTGGCTGTAGGAAGAGTTGGCTCTACCTCTGAAA
ACATCACACAGAAAGTAGTTTGGGTGGAAGAATCAGACAAACGGTCATTTCTGCTTGACC
TCCTAAATGCAACAGGCAAGGATTCAC TGACCTTAGTGTTTGTGGAGACCAAAAAGGGTG
CAGATTCTCTGGAGGATTTCTTATACCATGAAGGATACGCATGTACCAGCATCCATGGAG
ACCGTTCTCAGAGGGATAGAGAAGAGGCCCTTCAACAGTTCCGCTCAGGGA

Entry Created: Apr 19 1997
Last Updated: Apr 19 1997

COMMENTS

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

PUTATIVE ID Assigned by submitter
similar to RNA helicase

LIBRARY

Lib Name: HCC cell line (matastasis to liver in mouse) II
Organism: Homo sapiens
Tissue type: colon
Cell type: KM12SM
Cell line: KM12C(HCC)metastasis into mouse (liver)
Vector: pBluescript SK-
R. Site 1: EcoRI
R. Site 2: XhoI

SUBMITTER

Name: Kerlavage, AR
Lab: Bioinformatics

Institution: The Institute for Genomic Research
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Tel: 3018699056
Fax: 3018699423
E-mail: arkerlav@tigr.org

CITATIONS

Medline UID: 96026280
Title: Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Authors: Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., Venter,J.C.
Citation: Nature 377 (6547 Suppl): 3-174 1995

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CGCTCAGGATAGGAACTTCGCTAGAGGATCGGATCCCCGGGCTATTATATAGCTCGATCGATCT
TTCTCTATATTCGCGATATGGGATATATACACACACACATCGGCGATAGGATGACTGATCTA
CCCCATCT
CAGACACT

A6

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Details

1: T85890.yd58g05.r1 Soares...[gi:714242]

Links

IDENTIFIERS

dbEST Id: 156011
EST name: yd58g05.r1
GenBank Acc: T85890
GenBank gi: 714242
GDB Id: 468089

CLONE INFO

Clone Id: IMAGE:112472 (5')
Insert length: 1604
DNA type: cDNA

PRIMERS

Sequencing: M13RP1
PolyA Tail: Unknown

SEQUENCE

TTTTGCAAATACTTGGTGTAGATGAAGCTGATCGGATGTTGGATATGGGGTTTGAACCT
CAGATTTCGTAGAATAGTCGAACAAGATACTATGCCTCAAAGGGTGCCGCCACACTATG
ATGTTTGTAGTCTACTTTTCTAAGGAAATACAGATGCTGGCTCGTGATTTCTTAGGATGA
ATATATCTTCTTGGGCTGTAGGGAAGGAGTTGGGCTCTACCTCTGGAAAACATCACACAG
GAAAGTAGTTGGGGTGGGAAGGANTCAGGACAAACGGGTCATTTCTGGCTTGACCCTCCC
TAAATGGCAACAGGGGCAAGGGATTTCCTTGACCNTTAGGTGTTTGTGGGGGAGACCC
CAAAAGGGGGTGCCAGGNTTC

Quality: High quality sequence stops at base: 281

Entry Created: Mar 17 1995
Last Updated: Mar 17 1995

COMMENTS

Insert Size: 1604
High quality sequence stops: 281 Source: IMAGE Consortium,
LLNL This clone is available royalty-free through LLNL ;
contact the IMAGE Consortium (info@image.llnl.gov) for
further information.

PUTATIVE ID Assigned by submitter
SP:PL10_MOUSE P16381 PUTATIVE ATP-DEPENDENT RNA HELICASE ;

LIBRARY

Lib Name: Soares fetal liver spleen 1NFLS
Organism: Homo sapiens
Sex: male
Organ: Liver and Spleen
Develop. stage: 20 week-post conception fetus
Lab host: DH10B (ampicillin resistant)
Vector: pT7T3D (Pharmacia) with a modified polylinker
R. Site 1: Pac I
R. Site 2: Eco RI
Description: 1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

SUBMITTER

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Fax: 314 286 1810
E-mail: est@watson.wustl.edu

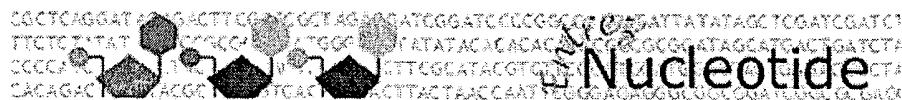
CITATIONS

Title: The WashU-Merck EST Project
Authors: Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., Wilson,R.
Year: 1995
Status: Unpublished

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1: T82153. yd95d08.r1 Soares...[gi:705160]

Links

```

fbEST Id: 147970
EST name: yd95d08.r1
GenBank Acc: T82153
GenBank gi: 705160
GDB Id: 471600

```

Clone Id: IMAGE:115983 (5')
Other ESTs on clone: yd95d08.s1
Insert length: 860
DNA type: cDNA

Sequencing: M13RP1
PolyA Tail: Unknown

TTTTGCAAATACTTGGTGTTAGATGAAGCTGATCGGATGTTGGATATGGGGTTTTGAGCCT
CAGATTCGTAGAATAGTCGAACAAGATACTATGCCTCCAAAGGGTGTCCGCCACACTATG
ATGTTTAGTGCTACTTTTCCTAAGGAAATACAGATGCTGGCTCGTGATTTCTTAGATGAA
TATATCTTCTTGGGCTGTAGGGAAGAGTTGGCTCTACCTCTGAAAACATCACACAGAAAG
TAGTTGGGGTGGGAAGGAATCAGACAAACGGTCATTTCTGGCTTGGACCTCCTAAATGGC
AACAGGGCAAGGGTTCACTTGACCTTAGTGTTTTGTTGGGAGACCCAAAAAGGGGTGCCA
G

Quality: High quality sequence stops at base: 269

Entry Created: Mar 10 1995
Last Updated: Mar 15 1995

Insert Size: 860
High quality sequence stops: 269 Source: IMAGE Consortium,
LLNL This clone is available royalty-free through LLNL ;
contact the IMAGE Consortium (info@image.llnl.gov) for
further information.

PUTATIVE ID Assigned by submitter
SP:PL10 MOUSE P16381 PUTATIVE ATP-DEPENDENT RNA HELICASE ;

```

Lib Name:      Soares fetal liver spleen 1NFLS
Organism:      Homo sapiens
Sex:           male
Organ:         Liver and Spleen
Develop. stage: 20 week-post conception fetus
Lab host:      DH10B (ampicillin resistant)
Vector:        pT7T3D (Pharmacia) with a modified polylinker
R. Site 1:     Pac I
R. Site 2:     Eco RI
Description:    1st strand cDNA was primed with a Pac I - oligo(dT) primer

```

[5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library went
through one round of normalization. Library constructed by
Bento Soares and M.Fatima Bonaldo.

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Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: The WashU-Merck EST Project
Authors: Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.,
Wilson, R.
Year: 1995
Status: Unpublished

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